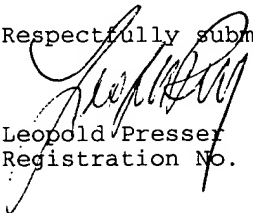


REMARKS

It is respectfully requested that this Preliminary Amendment be entered in this application prior to examination. Early and favorable consideration is requested.

Respectfully submitted,


Leopold Presser
Registration No. 19,827

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LP:ae

09037657.034088

SEQUENCE LISTING

<110> Hilton, Douglas J.
Nicola, Nicos A.
Farley, Alison
Wilson, Tracy
Zhang, Jian-Guo
Alexander, Warren
Rakar, Steven
Fabri, Louis
Kojima, Tetsuo
Maeda, Masatsugu
Kikuchi, Yasufumi
Nash, Andrew

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ENCODING SAME

<130> DAVIES COLLISON CAVE (CIP)

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<141> 1998-03-10

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ccc atg ccc gcg ggt cgc ccg gcc ccc gtc gcc caa tcc gcg cgg cgg 168
Met Pro Ala Gly Arg Pro Gly Pro Val Ala Gln Ser Ala Arg Arg
1 5 10 15
ccg ccg cgg ccg ctg tcc tcg ctg tgg tcg cct ctg ttg ctc tgt gtc 216
Pro Pro Arg Pro Leu Ser Ser Leu Trp Ser Pro Leu Leu Leu Cys Val
20 25 30
ctc ggg gtg cct cgg ggc gga tcg gga gcc cac aca gct gta atc agc 264
Leu Gly Val Pro Arg Gly Gly Ser Gly Ala His Thr Ala Val Ile Ser
35 40 45
ccc cag gac ccc acc ctt ctc atc gcc tcc tcc ctg caa gct acc tgc 312
Pro Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys
50 55 60

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acc	ctc	aat	ggt	cgc	cgc	ctg	ccc	tct	gag	ctg	tcc	cgc	ctc	ctt	aac	408
Thr	Leu	Asn	Gly	Arg	Arg	Leu	Pro	Ser	Glu	Leu	Ser	Arg	Leu	Leu	Asn	
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acc	tcc	acc	ctg	gcc	ctg	gcc	ctg	gct	aac	ctt	aat	ggg	tcc	agg	cag	456
Thr	Ser	Thr	Leu	Ala	Leu	Ala	Leu	Ala	Asn	Leu	Asn	Gly	Ser	Arg	Gln	
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cag	tca	gga	gac	aat	ctg	gtg	tgt	cac	gcc	cga	gac	ggc	agc	att	ctg	504
Gln	Ser	Gly	Asp	Asn	Leu	Val	Cys	His	Ala	Arg	Asp	Gly	Ser	Ile	Leu	
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Ala	Gly	Ser	Cys	Leu	Tyr	Val	Gly	Leu	Pro	Pro	Glu	Lys	Pro	Phe	Asn	
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Ile	Ser	Cys	Trp	Ser	Arg	Asn	Met	Lys	Asp	Leu	Thr	Cys	Arg	Trp	Thr	
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ccg	ggt	gca	cac	ggg	gag	aca	ttc	tta	cat	acc	aac	tac	tcc	ctc	aag	648
Pro	Gly	Ala	His	Gly	Glu	Thr	Phe	Leu	His	Thr	Asn	Tyr	Ser	Leu	Lys	
	160				165					170					175	
tac	aag	ctg	agg	tgg	tac	ggt	cag	gat	aac	aca	tgt	gag	gag	tac	cac	696
Tyr	Lys	Leu	Arg	Trp	Tyr	Gly	Gln	Asp	Asn	Thr	Cys	Glu	Glu	Tyr	His	
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act	gtg	ggc	cct	cac	tca	tgc	cat	atc	ccc	aag	gac	ctg	gcc	ctc	ttc	744
Thr	Val	Gly	Pro	His	Ser	Cys	His	Ile	Pro	Lys	Asp	Leu	Ala	Leu	Phe	
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act	ccc	tat	gag	atc	tgg	gtg	gaa	gcc	acc	aat	cgc	cta	ggc	tca	gca	792
Thr	Pro	Tyr	Glu	Ile	Trp	Val	Glu	Ala	Thr	Asn	Arg	Leu	Gly	Ser	Ala	
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Pro	Pro	Pro	Asp	Val	His	Val	Ser	Arg	Val	Gly	Gly	Leu	Glu	Asp	Gln	
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ctg	agt	gtg	cgc	tgg	gtc	tca	cca	cca	gct	ctc	aag	gat	ttc	ctc	ttc	936
Leu	Ser	Val	Arg	Trp	Val	Ser	Pro	Pro	Ala	Leu	Lys	Asp	Phe	Leu	Phe	
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caa	gcc	aag	tac	cag	atc	cgc	tac	cgc	gtg	gag	gac	agc	gtg	gac	tgg	984
Gln	Ala	Lys	Tyr	Gln	Ile	Arg	Tyr	Arg	Val	Glu	Asp	Ser	Val	Asp	Trp	
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aag	gtg	gtg	gat	gac	gtc	agc	aac	cag	acc	tcc	tgc	cgt	ctc	gcg	ggc	1032

Lys	Val	Val	Asp	Asp	Val	Ser	Asn	Gln	Thr	Ser	Cys	Arg	Leu	Ala	Gly		
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Gly	Ile	Tyr	Gly	Ser	Lys	Lys	Ala	Gly	Ile	Trp	Ser	Glu	Trp	Ser	His		
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ccc	acc	gct	gcc	tcc	acc	cct	cga	agt	gag	cgc	ccg	ggc	ccg	ggc	ggc	1176	
Pro	Thr	Ala	Ala	Ser	Thr	Pro	Arg	Ser	Glu	Arg	Pro	Gly	Pro	Gly	Gly		
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Arg	Glu	Leu	Lys	Gln	Phe	Leu	Gly	Trp	Leu	Lys	Lys	His	Ala	Tyr	Cys		
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 Val Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg Arg
 355 360 365
 Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser
 370 375 380
 Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln Lys
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 ccca atg ccc gcg ggt cgc ccg ggc ccc gtc gcc caa tcc gcg cgg cgg 169
 Met Pro Ala Gly Arg Pro Gly Pro Val Ala Gln Ser Ala Arg Arg
 1 5 10 15
 ccg ccg cgg ccg ctg tcc tcg ctg tgg tcg cct ctg ttg ctc tgt gtc 217
 Pro Pro Arg Pro Leu Ser Ser Leu Trp Ser Pro Leu Leu Leu Cys Val
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 Leu Gly Val Pro Arg Gly Gly Ser Gly Ala His Thr Ala Val Ile Ser
 35 40 45
 ccc cag gac ccc acc ctt ctc atc ggc tcc tcc ctg caa gct acc tgc 313
 Pro Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys
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 Ser Ile His Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp
 65 70 75
 acc ctc aat ggt cgc cgc ctg ccc tct gag ctg tcc cgc ctc ctt aac 409
 Thr Leu Asn Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn
 80 85 90 95

acc tcc acc ctg gcc ctg gcc ctg gct aac ctt aat ggg tcc agg cag	457
Thr Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln	
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Gln Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu	
115 120 125	
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Ala Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn	
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Ile Ser Cys Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr	
145 150 155	
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Pro Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys	
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Tyr Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His	
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Pro Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln	
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Gln Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp	
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Lys Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly	
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Leu Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe	
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 35 40 45
 Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser

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Leu	Asn	Gly	Arg	Arg 85	Leu	Pro	Ser	Glu	Leu 90	Ser	Arg	Leu	Leu	Asn 95	Thr
Ser	Thr	Leu	Ala 100	Leu	Ala	Leu	Ala	Asn 105	Leu	Asn	Gly	Ser	Arg	Gln 110	Gln
Ser	Gly	Asp 115	Asn	Leu	Val	Cys	His 120	Ala	Arg	Asp	Gly	Ser	Ile 125	Leu	Ala
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Ser 145	Cys	Trp	Ser	Arg	Asn 150	Met	Lys	Asp	Leu	Thr 155	Cys	Arg	Trp	Thr	Pro 160
Gly	Ala	His	Gly	Glu 165	Thr	Phe	Leu	His	Thr 170	Asn	Tyr	Ser	Leu	Lys 175	Tyr
Lys	Leu	Arg	Trp 180	Tyr	Gly	Gln	Asp	Asn 185	Thr	Cys	Glu	Glu	Tyr 190	His	Thr
Val	Gly 195	Pro	His	Ser	Cys	His	Ile 200	Pro	Lys	Asp	Leu	Ala 205	Leu	Phe	Thr
Pro	Tyr 210	Glu	Ile	Trp	Val	Glu 215	Ala	Thr	Asn	Arg	Leu 220	Gly	Ser	Ala	Arg
Ser 225	Asp	Val	Leu	Thr	Leu 230	Asp	Val	Leu	Asp	Val 235	Val	Thr	Thr	Asp	Pro 240
Pro	Pro	Asp	Val	His 245	Val	Ser	Arg	Val	Gly 250	Gly	Leu	Glu	Asp	Gln 255	Leu
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Ala	Lys 275	Tyr	Gln	Ile	Arg	Tyr	Arg 280	Val	Glu	Asp	Ser	Val 285	Asp	Trp	Lys
Val 290	Val	Asp	Asp	Val	Ser	Asn 295	Gln	Thr	Ser	Cys	Arg 300	Leu	Ala	Gly	Leu
Lys 305	Pro	Gly	Thr	Val	Tyr 310	Phe	Val	Gln	Val	Arg 315	Cys	Asn	Pro	Phe	Gly 320
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Thr	Ala	Ala	Ser 340	Thr	Pro	Arg	Ser	Glu 345	Arg	Pro	Gly	Pro	Gly 350	Gly	Gly
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Ser	His	Lys	Thr	Arg	Asn	Gln	Asp	Glu	Gly	Ile	Leu	Pro	Ser	Gly	Arg
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 Arg Thr Leu Leu Ser Lys His Arg Thr Arg Gly Ser Cys Pro Arg Ala
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 gac ggg gtg cgg cga gag gta agg ggg tct ggg tgagtggggc ctacagcagt 485
 Asp Gly Val Arg Arg Glu Val Arg Gly Ser Gly
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 <211> 155
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown Organism: Murine NR6.3

<400> 17
 Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly Ile Tyr
 1 5 10 15
 Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His Pro Thr Ala
 20 25 30
 Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly Val Cys
 35 40 45
 Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg Arg Glu Leu
 50 55 60
 Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser Asn Leu
 65 70 75 80
 Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln Lys Ser His
 85 90 95
 Lys Thr Arg Asn Gln Val Gly Lys Leu Gly Glu Ala Cys Val Gly Gly
 100 105 110

Lys Gly Ala Glu Glu Glu Arg Asp Pro Gly Glu Gln Pro Pro Gln His
115 120 125

Arg Thr Leu Leu Ser Lys His Arg Thr Arg Gly Ser Cys Pro Arg Ala
130 135 140

Asp Gly Val Arg Arg Glu Val Arg Gly Ser Gly
145 150 155

<210> 18

<211> 834

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(834)

<220>

<223> Description of Artificial Sequence: Nucleotide
sequence of products generated by 5' RACE of brain
cDNA using NR6 specific primers

<400> 18

ccc acc ctt ctc atc ggc tcc tcc ctg caa gct acc tgc tct ata cat 48
Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser Ile His
1 5 10 15

gga gac aca cct ggg gcc acc gct gag ggg ctc tac tgg acc ctc aat 96
Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr Leu Asn
20 25 30

ggt cgc cgc ctg ccc tct gag ctg tcc cgc ctc ctt aac acc tcc acc 144
Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn Thr Ser Thr
35 40 45

ctg gcc ctg gcc ctg gct aac ctt aat ggg tcc agg cag cag tca gga 192
Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln Gln Ser Gly
50 55 60

gac aat ctg gtg tgt cac gcc cga gac ggc agc att ctg gct ggc tcc 240
Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala Gly Ser
65 70 75 80

tgc ctc tat gtt ggc ttg ccc cct gag aag ccc ttt aac atc agc tgc 288
Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn Ile Ser Cys
85 90 95

tgg tcc cgg aac atg aag gat ctc acg tgc cgc tgg aca ccg ggt gca 336
Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr Pro Gly Ala
100 105 110

cac ggg gag aca ttc tta cat acc aac tac tcc ctc aag tac aag ctg 384
His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys Tyr Lys Leu
115 120 125

agg tgg tac ggt cag gat aac aca tgt gag gag tac cac act gtg ggg	432
Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His Thr Val Gly	
130 135 140	
ccc cac tca tgc cat atc ccc aag gac ctg gcc ctc ttc act ccc tat	480
Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe Thr Pro Tyr	
145 150 155 160	
gag atc tgg gtg gaa gcc acc aat cgc cta ggc tca gca aga tct gat	528
Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala Arg Ser Asp	
165 170 175	
gtc ctc aca ctg gat gtc ctg gac gtg gtg acc acg gac ccc cca ccc	576
Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp Pro Pro Pro	
180 185 190	
gac gtg cac gtg agc cgc gtt ggg ggc ctg gag gac cag ctg agt gtg	624
Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln Leu Ser Val	
195 200 205	
cgc tgg gtc tca cca cca gct ctc aag gat ttc ctc ttc caa gcc aag	672
Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe Gln Ala Lys	
210 215 220	
tac cag atc cgc tac cgc gtg gag gac agc gtg gac tgg aag gtg gtg	720
Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp Lys Val Val	
225 230 235 240	
gat gac gtc agc aac cag acc tcc tgc cgt ctc gcg ggc ctg aag ccc	768
Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly Leu Lys Pro	
245 250 255	
ggc acc gtt tac ttc gtc caa gtg cgt tgt aac cca ttc ggg atc tat	816
Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly Ile Tyr	
260 265 270	
ggg tcg aaa aag gcg gga	834
Gly Ser Lys Lys Ala Gly	
275	

<210> 19

<211> 278

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Haemopoietin receptor

<400> 19

Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser Ile His
1 5 10 15

Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr Leu Asn
20 25 30

Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn Thr Ser Thr

35					40					45					
Leu	Ala	Leu	Ala	Leu	Ala	Asn	Leu	Asn	Gly	Ser	Arg	Gln	Gln	Ser	Gly
	50					55					60				
Asp	Asn	Leu	Val	Cys	His	Ala	Arg	Asp	Gly	Ser	Ile	Leu	Ala	Gly	Ser
65					70					75					80
Cys	Leu	Tyr	Val	Gly	Leu	Pro	Pro	Glu	Lys	Pro	Phe	Asn	Ile	Ser	Cys
				85					90					95	
Trp	Ser	Arg	Asn	Met	Lys	Asp	Leu	Thr	Cys	Arg	Trp	Thr	Pro	Gly	Ala
			100					105					110		
His	Gly	Glu	Thr	Phe	Leu	His	Thr	Asn	Tyr	Ser	Leu	Lys	Tyr	Lys	Leu
		115					120					125			
Arg	Trp	Tyr	Gly	Gln	Asp	Asn	Thr	Cys	Glu	Glu	Tyr	His	Thr	Val	Gly
	130					135					140				
Pro	His	Ser	Cys	His	Ile	Pro	Lys	Asp	Leu	Ala	Leu	Phe	Thr	Pro	Tyr
145					150					155					160
Glu	Ile	Trp	Val	Glu	Ala	Thr	Asn	Arg	Leu	Gly	Ser	Ala	Arg	Ser	Asp
				165					170					175	
Val	Leu	Thr	Leu	Asp	Val	Leu	Asp	Val	Val	Thr	Thr	Asp	Pro	Pro	Pro
			180					185					190		
Asp	Val	His	Val	Ser	Arg	Val	Gly	Gly	Leu	Glu	Asp	Gln	Leu	Ser	Val
		195					200					205			
Arg	Trp	Val	Ser	Pro	Pro	Ala	Leu	Lys	Asp	Phe	Leu	Phe	Gln	Ala	Lys
	210					215					220				
Tyr	Gln	Ile	Arg	Tyr	Arg	Val	Glu	Asp	Ser	Val	Asp	Trp	Lys	Val	Val
225					230					235					240
Asp	Asp	Val	Ser	Asn	Gln	Thr	Ser	Cys	Arg	Leu	Ala	Gly	Leu	Lys	Pro
				245					250					255	
Gly	Thr	Val	Tyr	Phe	Val	Gln	Val	Arg	Cys	Asn	Pro	Phe	Gly	Ile	Tyr
			260					265					270		
Gly	Ser	Lys	Lys	Ala	Gly										
		275													

<210> 20
 <211> 143
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> CDS
 <222> (105)..(143)

<220>

<223> Description of Artificial Sequence:Nucleotide
sequence unique to 5' RACE of brain cDNA

<400> 20

ggcatgaagg cttaggggtgg ggatcggtag gacccatgca cccagagaaa gggactgggtg 60
gcaactttca aactctctgg ggaaggaaga agggctgaaa gagg atg aac ggg ctc 116
Met Asn Gly Leu
1

aga cac agc tgt aat cag ccc cca gga 143
Arg His Ser Cys Asn Gln Pro Pro Gly
5 10

<210> 21

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino Acid Sequence encoded
by Nucleotide sequence unique to 5' RACE of brain cDNA

<400> 21

Met Asn Gly Leu Arg His Ser Cys Asn Gln Pro Pro Gly
1 5 10

<210> 22

<211> 1930

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism:Murine NR6

<400> 22

ggcacgagct tcgctgtccg cgcccagtga cgcgcggtgcg gacccgagcc ccaatctgca 60
ccccgcagac tcgccccgcg ccataaccgg cgttgcagtc accgcccgtt gcgcgccacc 120
cccaatgccc gcggggtcgc cgggccccgt cgcccaatcc gcgcggcggc gcgcgcggcc 180
gctgtcctcg ctgtggtcgc ctctgttgct ctgtgtcctc ggggtgcctc ggggcggatc 240
gggagcccac acagctgtaa tcagccccca ggaccccacc cttctcatcg gtcctcctcct 300
gcaagctacc tgctctatac atggagacac acctggggcc accgctgagg ggctctactg 360
gaccctcaat ggtgcgcgcc tgccctctga gctgtccgcg ctccttaaca cctccaccct 420
ggccctggcc ctggctaacc ttaatgggtc caggcagcag tcaggagaca atctggtgtg 480
tcacgcccga gacggcagca ttctgggttg ctctgcctc tatgttggtg tgccccctga 540

gaagcccttt aacatcagct gctgggtcccg gaacatgaag gatctcacgt gccgctggac 600
 accgggtgca cacggggaga cattcttaca taccaactac tccctcaagt acaagctgag 660
 gtggtacggt caggataaca catgtgagga gtaccacact gtgggccctc actcatgcca 720
 tatccccaag gacctggccc tcttcactcc ctatgagatc tgggtggaag ccaccaatcg 780
 cctaggetca gcaagatctg atgtcctcac actggatgtc ctggacgtgg tgaccacgga 840
 cccccaccc gacgtgcacg tgagccgctg tgggggctg gaggaccagc tgagtgtgcg 900
 ctgggtctca ccaccagctc tcaaggattt cctcttccaa gccaaagtacc agatccgcta 960
 ccgctgggag gacagcgtgg actggaaggt ggtggatgac gtcagcaacc agacctcctg 1020
 ccgtctcgcg ggcctgaagc ccggcaccgt ttacttcgtc caagtgcgtt gtaaccatt 1080
 cgggatctat gggctgaaaa aggcgggaat ctggagcgag tggagccacc ccaccgctgc 1140
 ctccaccct cgaagtgagc gcccgggccc gggcgggcgg gtgtgcgagc cgcggggcgg 1200
 cgagcccagc tcggggcccg tgcggcgcg gctcaagcag ttcctcggct ggctcaagaa 1260
 gcacgcatac tgctcgaacc ttagtttccg cctgtacgac cagtggcgtg cttggatgca 1320
 gaagtcacac aagacccgaa accaggtagg aaagttgggg gaggcttgcg tggggggtaa 1380
 aggagcagag gaagagagag acccggtga gcagcctcca caacaccgca ctcttctttc 1440
 caagcacagg acgaggggat cctgccctcg ggcagacggg gtgcggcgag aggtaagggg 1500
 gtctgggtga gtggggccta cagcagtcta gatgaggccc tttcccctcc ttcggtgttg 1560
 ctcaaaggga tctcttagtg ctcatctcac ccactgcaaa gagccccagg ttttactgca 1620
 tcatcaagtt gctgaagggt ccaggcttaa tgtggcctct tttctgccct caggtcctgc 1680
 cggctaaact ctaaggatag gccatcctcc tgctgggtca gacctggagg ctacactgaa 1740
 ttggagcccc tctgtaccta tctgggcaac aaagaaacct accatgaggc tggggcaciaa 1800
 tgagctccca caaccacagc tttgggtccac atgatgggtca cacttgata taccacagt 1860
 tgggtaaggt tgggggtattg cagggcctcc caacaatctc tttaaataaa taaaggagtt 1920
 gttcaggtaa 1930

<210> 23

<211> 560

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR product for human NR6

<400> 23
 tccaggcagc ggtcggggga caacctcgtg tgccacgccc gtgacggcag catcctggct 60
 ggctcctgcc tctatgttgg cctgccccca gagaaacccg tcaacatcag ctgctgggtcc 120
 aagaacatga aggacttgac ctgccgctgg acgccagggg cccacgggga gaccttcctc 180
 cacaccaact actccctcaa gtacaagctt aggtgggtatg gccaggacaa cacatgtgag 240
 gagtaccaca cagtggggcc ccaactcctgc cacatcccca aggacctggc tctctttacg 300
 ccctatgaga tctgggtgga ggccaccaac cgcttgggct ctgcccgtc cgatgtactc 360
 acgctggata tcctggatgt ggtgaccacg gacccccgc ccgacgtgca cgtgagccgc 420
 gtcggggggc tggaggacca gctgagcgtg cgctgggtgt cgccaccgc cctcaaggat 480
 ttcctttttc aagccaaata ccagatccgc taccgagtgg aggacagtgt ggaatggaag 540
 gtggtggacg atgtgagcaa 560

<210> 24
 <211> 1391
 <212> DNA
 <213> Unknown

<220>
 <221> CDS
 <222> (1)..(1050)

<220>
 <223> Description of Unknown Organism:Nucleotide
 sequence of clone HFK-66 encoding human NR6

<400> 24
 acc ctc aac ggg cgc cgc ctg ccc cct gag ctc tcc cgt gta ctc aac 48
 Thr Leu Asn Gly Arg Arg Leu Pro Pro Glu Leu Ser Arg Val Leu Asn
 1 5 10 15
 gcc tcc acc ttg gct ctg gcc ctg gcc aac ctc aat ggg tcc agg cag 96
 Ala Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln
 20 25 30
 cgg tcg ggg gac aac ctc gtg tgc cac gcc cgt gac ggc agc atc ctg 144
 Arg Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu
 35 40 45
 gct ggc tcc tgc ctc tat gtt ggc ctg ccc cca gag aaa ccc gtc aac 192
 Ala Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Val Asn
 50 55 60
 atc agc tgc tgg tcc aag aac atg aag gac ttg acc tgc cgc tgg acg 240
 Ile Ser Cys Trp Ser Lys Asn Met Lys Asp Leu Thr Cys Arg Trp Thr
 65 70 75 80
 cca ggg gcc cac ggg gag acc ttc ctc cac acc aac tac tcc ctc aag 288

Pro	Gly	Ala	His	Gly	Glu	Thr	Phe	Leu	His	Thr	Asn	Tyr	Ser	Leu	Lys	
				85					90					95		
tac	aag	ctt	agg	tgg	tat	ggc	cag	gac	aac	aca	tgt	gag	gag	tac	cac	336
Tyr	Lys	Leu	Arg	Trp	Tyr	Gly	Gln	Asp	Asn	Thr	Cys	Glu	Glu	Tyr	His	
			100					105					110			
aca	gtg	ggg	ccc	cac	tcc	tgc	cac	atc	ccc	aag	gac	ctg	gct	ctc	ttt	384
Thr	Val	Gly	Pro	His	Ser	Cys	His	Ile	Pro	Lys	Asp	Leu	Ala	Leu	Phe	
		115					120					125				
acg	ccc	tat	gag	atc	tgg	gtg	gag	gcc	acc	aac	cgc	ctg	ggc	tct	gcc	432
Thr	Pro	Tyr	Glu	Ile	Trp	Val	Glu	Ala	Thr	Asn	Arg	Leu	Gly	Ser	Ala	
	130					135					140					
cgc	tcc	gat	gta	ctc	acg	ctg	gat	atc	ctg	gat	gtg	gtg	acc	acg	gac	480
Arg	Ser	Asp	Val	Leu	Thr	Leu	Asp	Ile	Leu	Asp	Val	Val	Thr	Thr	Asp	
145					150					155					160	
ccc	ccg	ccc	gac	gtg	cac	gtg	agc	cgc	gtc	ggg	ggc	ctg	gag	gac	cag	528
Pro	Pro	Pro	Asp	Val	His	Val	Ser	Arg	Val	Gly	Gly	Leu	Glu	Asp	Gln	
				165					170					175		
ctg	agc	gtg	cgc	tgg	gtg	tgc	cca	ccc	gcc	ctc	aag	gat	ttc	ctc	ttt	576
Leu	Ser	Val	Arg	Trp	Val	Ser	Pro	Pro	Ala	Leu	Lys	Asp	Phe	Leu	Phe	
			180					185					190			
caa	gcc	aaa	tac	cag	atc	cgc	tac	cga	gtg	gag	gac	agt	gtg	gac	tgg	624
Gln	Ala	Lys	Tyr	Gln	Ile	Arg	Tyr	Arg	Val	Glu	Asp	Ser	Val	Asp	Trp	
		195					200					205				
aag	gtg	gtg	gac	gat	gtg	agc	aac	cag	acc	tcc	tgc	cgc	ctg	gcc	ggc	672
Lys	Val	Val	Asp	Asp	Val	Ser	Asn	Gln	Thr	Ser	Cys	Arg	Leu	Ala	Gly	
	210					215					220					
ctg	aaa	ccc	ggc	acc	gtg	tac	ttc	gtg	caa	gtg	cgc	tgc	aac	ccc	ttt	720
Leu	Lys	Pro	Gly	Thr	Val	Tyr	Phe	Val	Gln	Val	Arg	Cys	Asn	Pro	Phe	
225					230					235					240	
ggc	atc	tat	ggc	tcc	aag	aaa	gcc	ggg	atc	tgg	agt	gag	tgg	agc	cac	768
Gly	Ile	Tyr	Gly	Ser	Lys	Lys	Ala	Gly	Ile	Trp	Ser	Glu	Trp	Ser	His	
				245					250					255		
ccc	aca	gcc	gcc	tcc	act	ccc	cgc	agt	gag	cgc	ccg	ggc	ccg	ggc	ggc	816
Pro	Thr	Ala	Ala	Ser	Thr	Pro	Arg	Ser	Glu	Arg	Pro	Gly	Pro	Gly	Gly	
			260					265					270			
ggg	gcg	tgc	gaa	ccg	cgg	ggc	gga	gag	ccg	agc	tgc	ggg	ccg	gtg	cgg	864
Gly	Ala	Cys	Glu	Pro	Arg	Gly	Gly	Glu	Pro	Ser	Ser	Gly	Pro	Val	Arg	
		275					280					285				
cgc	gag	ctc	aag	cag	ttc	ctg	ggc	tgg	ctc	aag	aag	cac	gcg	tac	tgc	912
Arg	Glu	Leu	Lys	Gln	Phe	Leu	Gly	Trp	Leu	Lys	Lys	His	Ala	Tyr	Cys	
	290					295					300					
tcc	aac	ctc	agc	ttc	cgc	ctc	tac	gac	cag	tgg	cga	gcc	tgg	atg	cag	960
Ser	Asn	Leu	Ser	Phe	Arg	Leu	Tyr	Asp	Gln	Trp	Arg	Ala	Trp	Met	Gln	

305			310			315			320								
aag	tcg	cac	aag	acc	cgc	aac	cag	cac	agg	acg	agg	gga	tcc	tgc	cct	1008	
Lys	Ser	His	Lys	Thr	Arg	Asn	Gln	His	Arg	Thr	Arg	Gly	Ser	Cys	Pro		
				325						330				335			
cgg	gca	gac	ggg	gca	cgg	cga	gag	gtc	ctg	cca	gat	aag	ctg			1050	
Arg	Ala	Asp	Gly	Ala	Arg	Arg	Glu	Val	Leu	Pro	Asp	Lys	Leu				
				340						345				350			
taggggctca			ggccaccctc			cctgccacgt			ggagacgcag			aggccgaacc			caaactgggg		1110
ccacctctgt			accctcactt			cagggcacct			gagcccctca			gcaggagctg			gggtggcccc		1170
tgagctccaa			cggccataac			agctctgact			cccacgtgag			gccacctttg			ggtgcacccc		1230
agtgggtgtg			tgtgtgtgtg			tgagggtttg			ttgagttgcc			tagaaccctt			gccagggctg		1290
ggggtgagaa			ggggagtcac			tactccccat			tacctagggc			ccctccaaaa			gagtcctttt		1350
aaataaatga			gctattttaqg			tgcaaaaaaaaa			aaaaaaaaaaaa			a					1391

130					135					140					
Arg	Ser	Asp	Val	Leu	Thr	Leu	Asp	Ile	Leu	Asp	Val	Val	Thr	Thr	Asp
145					150					155					160
Pro	Pro	Pro	Asp	Val	His	Val	Ser	Arg	Val	Gly	Gly	Leu	Glu	Asp	Gln
				165					170					175	
Leu	Ser	Val	Arg	Trp	Val	Ser	Pro	Pro	Ala	Leu	Lys	Asp	Phe	Leu	Phe
			180					185					190		
Gln	Ala	Lys	Tyr	Gln	Ile	Arg	Tyr	Arg	Val	Glu	Asp	Ser	Val	Asp	Trp
		195					200					205			
Lys	Val	Val	Asp	Asp	Val	Ser	Asn	Gln	Thr	Ser	Cys	Arg	Leu	Ala	Gly
	210					215					220				
Leu	Lys	Pro	Gly	Thr	Val	Tyr	Phe	Val	Gln	Val	Arg	Cys	Asn	Pro	Phe
225					230					235					240
Gly	Ile	Tyr	Gly	Ser	Lys	Lys	Ala	Gly	Ile	Trp	Ser	Glu	Trp	Ser	His
				245					250					255	
Pro	Thr	Ala	Ala	Ser	Thr	Pro	Arg	Ser	Glu	Arg	Pro	Gly	Pro	Gly	Gly
			260					265					270		
Gly	Ala	Cys	Glu	Pro	Arg	Gly	Gly	Glu	Pro	Ser	Ser	Gly	Pro	Val	Arg
		275					280					285			
Arg	Glu	Leu	Lys	Gln	Phe	Leu	Gly	Trp	Leu	Lys	Lys	His	Ala	Tyr	Cys
	290					295					300				
Ser	Asn	Leu	Ser	Phe	Arg	Leu	Tyr	Asp	Gln	Trp	Arg	Ala	Trp	Met	Gln
305					310					315					320
Lys	Ser	His	Lys	Thr	Arg	Asn	Gln	His	Arg	Thr	Arg	Gly	Ser	Cys	Pro
				325					330					335	
Arg	Ala	Asp	Gly	Ala	Arg	Arg	Glu	Val	Leu	Pro	Asp	Lys	Leu		
			340					345					350		

<210> 26

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:UP1
Oligonucleotide

<400> 26

tccaggcagc ggctcggggga caac

24

<210> 27

<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:LP1
Oligonucleotide

<400> 27
ttgctcacat cgtccaccac cttc

24

<210> 28
<211> 6663
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown Organism:Murine NR6 gene

<400> 28
cccagaactc ttggacgctg aggcaggagg attcccaagt ttcaagacag tgtgttttcta 60
ggtaatgaga ccctgtcaag aaaagaaaag aaataaagag acaagaaaat gtttataggc 120
tgtgagacag cttggtgggt aaggggcact tgcctccaat caagatgacc tcagcccat 180
ccctaggaat ccatggtaga aggagaaagc aaactcgcag ctgctgacct ccatacatgt 240
gctccaatgt gcacacacac agggagacat aatcaattaa taggatgtat ttgcttagat 300
ttgagtaggc atttatgact gatgttttaa aatttttatt tgattttatg aaaatatacc 360
tgtttgtatt tggtttggtt tggtttgagt tttgtttatt tgagacaggg cttctctgtg 420
tagtcctggc tgtccttgga actcactctg tagaccaggc tggccttgaa ctcagaaatc 480
cgctgcttg tgcctcccaa gtgcttagat taaagggtgtg cactgccatt cagcaaaatt 540
gcatacttta accccagtat ttgggaggca gaggcagact aatgtgtgaa ttccaggcta 600
gccaaggata cagagtgaga ccctattctt accctcccc cccaaaacc caaatgtat 660
tttgtgcttg tgtatgtaca tgtgtgttgc agcacgtaaa tgtccaagga caacttgtag 720
aagttctctc cgttcacagt ctaagtcctg aattcaaact aaggtcctca ggcttagcca 780
cagtcttctt tatgtactga gccatttcac tggccctgga ttgactgatg aattaatttt 840
tgagataagg tctctttagt ctctagctag gctcaaacta tgaactccca aggtcatctt 900
gagctgctgg tactcttgct tccaccccaa gtggtggaat gatactcagg cagcacttct 960
ctggggaagg ggctggcctt ggccttgatt ttgttgctc agcttcaatg agtgcttggg 1020
tctcgttgtt tcttttcttt atctgtgaaa tgggtgaaca cctgttcaag acttctgac 1080
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 acttgatat accccagtgt gggtaggggt ggggtattgc agggcctccc aagagtctct 11760
 ttaaataaat aaaggagttg ttcaggctcc gatggccagt gtgtttgggg cctatgtgct 11820
 ggggtggggg ga 11832

<210> 39
 <211> 26
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Murine peptide

<400> 39
 Val Ile Ser Pro Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln
 1 5 10 15
 Ala Thr Cys Ser Ile His Gly Asp Thr Pro
 20 25

<210> 40
 <211> 21
 <212> DNA
 <213> Oligonucleotide Sequence

<400> 40
 gtccaagtgc gttgtaaccc a 21

<210> 41
 <211> 24
 <212> DNA
 <213> Oligonucleotide Sequence

<400> 41
 gctgagtgtg cgctgggtct cacc 24

<210> 42
 <211> 18
 <212> DNA
 <213> Oligonucleotide Sequence

<400> 42
ggctccactc gctccaga

18

<210> 43
<211> 2079
<212> DNA
<213> Unknown

<220>
<221> CDS
<222> (513)..(1775)

<220>
<223> Description of Unknown Organism: Nucleotide Sequence of NR6

<400> 43
gcggtatttg tgtttcaaat ctatctacag aaaagattga gaaccagaag cccttttcgt 60

tttttgaaag ctagctgact cactgttcaa gaaaggagaa cactttcaat tatgctgttt 120

gactgcagtg tcagggatcc aaaggaaatg actccatccc ttccttttca tcccaacctc 180

agtgcacgca aattctgatg tgactgaggg ttggcttggtg aaggagtcac taggaaattc 240

tgcctaagcc atagcgcgat gagaaggatg taccctatgg tggtagatttt cctgtgcccc 300

ctcagaggaa agttgtcaga tgagcaggtg gaggatttcta tagcaaacag caagctaata 360

ggttacacag ataactctct gactttgcct tacagaacct gtgctattga ccttagggca 420

aggttcatgc tcagggggcc aactctgtgg gttaggattt gagtttaagc agcttctgct 480

catatttcag cgcccccggc agcgccggcc cc atg ccc gcc ggc cgc cgg ggc 533
Met Pro Ala Gly Arg Arg Gly
1 5

ccc gcc gcc caa tcc gcg cgg cgg ccg ccg ccg ttg ctg ccc ctg ctg 581
Pro Ala Ala Gln Ser Ala Arg Arg Pro Pro Pro Leu Leu Pro Leu Leu
10 15 20

ctg ctc tgc gtc ctc ggg gcg ccg cga gcc gga tca gga gcc cac aca 629
Leu Leu Cys Val Leu Gly Ala Pro Arg Ala Gly Ser Gly Ala His Thr
25 30 35

gct gtg atc agt ccc cag gat ccc acg ctt ctc atc ggc tcc tcc ctg	677
Ala Val Ile Ser Pro Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu	
40 45 50 55	
ctg gcc acc tgc tca gtg cac gga gac cca cca gga gcc acc gcc gag	725
Leu Ala Thr Cys Ser Val His Gly Asp Pro Pro Gly Ala Thr Ala Glu	
60 65 70	
ggc ctc tac tgg acc ctc aat ggg cgc cgc ctg ccc cct gag ctc tcc	773
Gly Leu Tyr Trp Thr Leu Asn Gly Arg Arg Leu Pro Pro Glu Leu Ser	
75 80 85	
cgt gta ctc aac gcc tcc acc ttg gct ctg gcc ctg gcc aac ctc aat	821
Arg Val Leu Asn Ala Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn	
90 95 100	
ggg tcc agg cag cgg tgc ggg gac aac ctc gtg tgc cac gcc cgt gac	869
Gly Ser Arg Gln Arg Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp	
105 110 115	
ggc agc atc ctg gct ggc tcc tgc ctc tat gtt ggc ctg ccc cca gag	917
Gly Ser Ile Leu Ala Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu	
120 125 130 135	
aaa ccc gtc aac atc agc tgc tgg tcc aag aac atg aag gac ttg acc	965
Lys Pro Val Asn Ile Ser Cys Trp Ser Lys Asn Met Lys Asp Leu Thr	
140 145 150	
tgc cgc tgg acg cca ggg gcc cac ggg gag acc ttc ctc cac acc aac	1013
Cys Arg Trp Thr Pro Gly Ala His Gly Glu Thr Phe Leu His Thr Asn	
155 160 165	
tac tcc ctc aag tac aag ctt agg tgg tat ggc cag gac aac aca tgt	1061
Tyr Ser Leu Lys Tyr Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys	
170 175 180	
gag gag tac cac aca gtg ggg ccc cac tcc tgc cac atc ccc aag gac	1109
Glu Glu Tyr His Thr Val Gly Pro His Ser Cys His Ile Pro Lys Asp	
185 190 195	
ctg gct ctc ttt acg ccc tat gag atc tgg gtg gag gcc acc aac cgc	1157
Leu Ala Leu Phe Thr Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg	
200 205 210 215	
ctg ggc tct gcc cgc tcc gat gta ctc acg ctg gat atc ctg gat gtg	1205

Leu	Gly	Ser	Ala	Arg 220	Ser	Asp	Val	Leu	Thr 225	Leu	Asp	Ile	Leu	Asp 230	Val		
gtg	acc	acg	gac	ccc	ccg	ccc	gac	gtg	cac	gtg	agc	cgc	gtc	ggg	ggc	1253	
Val	Thr	Thr	Asp 235	Pro	Pro	Pro	Asp	Val 240	His	Val	Ser	Arg	Val 245	Gly	Gly		
ctg	gag	gac	cag	ctg	agc	gtg	cgc	tgg	gtg	tcg	cca	ccc	gcc	ctc	aag	1301	
Leu	Glu	Asp 250	Gln	Leu	Ser	Val	Arg 255	Trp	Val	Ser	Pro	Pro	Ala	Leu	Lys		
gat	ttc	ctc	ttt	caa	gcc	aaa	tac	cag	atc	cgc	tac	cga	gtg	gag	gac	1349	
Asp	Phe 265	Leu	Phe	Gln	Ala	Lys 270	Tyr	Gln	Ile	Arg	Tyr 275	Arg	Val	Glu	Asp		
agt	gtg	gac	tgg	aag	gtg	gtg	gac	gat	gtg	agc	aac	cag	acc	tcc	tgc	1397	
Ser 280	Val	Asp	Trp	Lys	Val 285	Val	Asp	Asp	Val	Ser 290	Asn	Gln	Thr	Ser	Cys 295		
cgc	ctg	gcc	ggc	ctg	aaa	ccc	ggc	acc	gtg	tac	ttc	gtg	caa	gtg	cgc	1445	
Arg	Leu	Ala	Gly	Leu 300	Lys	Pro	Gly	Thr	Val 305	Tyr	Phe	Val	Gln	Val 310	Arg		
tgc	aac	ccc	ttt	ggc	atc	tat	ggc	tcc	aag	aaa	gcc	ggg	atc	tgg	agt	1493	
Cys	Asn	Pro	Phe 315	Gly	Ile	Tyr	Gly	Ser 320	Lys	Lys	Ala	Gly	Ile 325	Trp	Ser		
gag	tgg	agc	cac	ccc	aca	gcc	gcc	tcc	act	ccc	cgc	agt	gag	cgc	ccg	1541	
Glu	Trp	Ser 330	His	Pro	Thr	Ala	Ala 335	Ser	Thr	Pro	Arg	Ser 340	Glu	Arg	Pro		
ggc	ccg	ggc	ggc	ggg	gcg	tgc	gaa	ccg	cgg	ggc	gga	gag	ccg	agc	tcg	1589	
Gly	Pro 345	Gly	Gly	Gly	Ala	Cys 350	Glu	Pro	Arg	Gly	Gly 355	Glu	Pro	Ser	Ser		
ggg	ccg	gtg	cgg	cgc	gag	ctc	aag	cag	ttc	ctg	ggc	tgg	ctc	aag	aag	1637	
Gly 360	Pro	Val	Arg	Arg	Glu 365	Leu	Lys	Gln	Phe	Leu 370	Gly	Trp	Leu	Lys	Lys 375		
cac	gcg	tac	tgc	tcc	aac	ctc	agc	ttc	cgc	ctc	tac	gac	cag	tgg	cga	1685	
His	Ala	Tyr	Cys	Ser 380	Asn	Leu	Ser	Phe	Arg 385	Leu	Tyr	Asp	Gln	Trp 390	Arg		
gcc	tgg	atg	cag	aag	tcg	cac	aag	acc	cgc	aac	cag	gac	gag	ggg	atc	1733	
Ala	Trp	Met	Gln 395	Lys	Ser	His	Lys	Thr 400	Arg	Asn	Gln	Asp	Glu 405	Gly	Ile		

ctg ccc tcg ggc aga cgg ggc acg gcg aga ggt cct gcc aga 1775
 Leu Pro Ser Gly Arg Arg Gly Thr Ala Arg Gly Pro Ala Arg
 410 415 420
 taagctgtag gggctcaggc caccctccct gccacgtgga gacgcagagg ccgaacccaa 1835
 actggggcca cctctgtacc ctcacttcag ggcacctgag ccaccctcag caggagctgg 1895
 ggtggcccct gagctccaac ggccataaca gctctgactc ccacgtgagg ccacctttgg 1955
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 atcc 2079

<210> 44
 <211> 421
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown Organism: Amino Acid Sequence of NR6

<400> 44
 Met Pro Ala Gly Arg Arg Gly Pro Ala Ala Gln Ser Ala Arg Arg Pro
 1 5 10 15
 Pro Pro Leu Leu Pro Leu Leu Leu Leu Cys Val Leu Gly Ala Pro Arg
 20 25 30
 Ala Gly Ser Gly Ala His Thr Ala Val Ile Ser Pro Gln Asp Pro Thr
 35 40 45
 Leu Leu Ile Gly Ser Ser Leu Leu Ala Thr Cys Ser Val His Gly Asp
 50 55 60
 Pro Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr Leu Asn Gly Arg
 65 70 75 80
 Arg Leu Pro Pro Glu Leu Ser Arg Val Leu Asn Ala Ser Thr Leu Ala
 85 90 95
 Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln Arg Ser Gly Asp Asn
 100 105 110
 Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala Gly Ser Cys Leu
 115 120 125
 Tyr Val Gly Leu Pro Pro Glu Lys Pro Val Asn Ile Ser Cys Trp Ser

130				135				140							
Lys 145	Asn	Met	Lys	Asp	Leu 150	Thr	Cys	Arg	Trp	Thr 155	Pro	Gly	Ala	His	Gly 160
Glu	Thr	Phe	Leu	His 165	Thr	Asn	Tyr	Ser	Leu 170	Lys	Tyr	Lys	Leu	Arg	Trp 175
Tyr	Gly	Gln	Asp	Asn 180	Thr	Cys	Glu	Glu 185	Tyr	His	Thr	Val	Gly 190	Pro	His
Ser	Cys	His 195	Ile	Pro	Lys	Asp	Leu 200	Ala	Leu	Phe	Thr	Pro	Tyr	Glu	Ile
Trp	Val 210	Glu	Ala	Thr	Asn	Arg 215	Leu	Gly	Ser	Ala	Arg 220	Ser	Asp	Val	Leu
Thr 225	Leu	Asp	Ile	Leu	Asp 230	Val	Val	Thr	Thr	Asp 235	Pro	Pro	Pro	Asp	Val 240
His	Val	Ser	Arg	Val 245	Gly	Gly	Leu	Glu	Asp 250	Gln	Leu	Ser	Val	Arg	Trp 255
Val	Ser	Pro	Pro	Ala 260	Leu	Lys	Asp	Phe 265	Leu	Phe	Gln	Ala	Lys 270	Tyr	Gln
Ile	Arg	Tyr 275	Arg	Val	Glu	Asp	Ser 280	Val	Asp	Trp	Lys	Val 285	Val	Asp	Asp
Val 290	Ser	Asn	Gln	Thr	Ser	Cys 295	Arg	Leu	Ala	Gly	Leu 300	Lys	Pro	Gly	Thr
Val 305	Tyr	Phe	Val	Gln	Val 310	Arg	Cys	Asn	Pro	Phe 315	Gly	Ile	Tyr	Gly	Ser 320
Lys	Lys	Ala	Gly	Ile 325	Trp	Ser	Glu	Trp	Ser 330	His	Pro	Thr	Ala	Ala	Ser 335
Thr	Pro	Arg	Ser 340	Glu	Arg	Pro	Gly	Pro 345	Gly	Gly	Gly	Ala	Cys 350	Glu	Pro
Arg	Gly	Gly 355	Glu	Pro	Ser	Ser	Gly 360	Pro	Val	Arg	Arg	Glu 365	Leu	Lys	Gln
Phe 370	Leu	Gly	Trp	Leu	Lys	Lys 375	His	Ala	Tyr	Cys	Ser 380	Asn	Leu	Ser	Phe
Arg 385	Leu	Tyr	Asp	Gln	Trp 390	Arg	Ala	Trp	Met	Gln 395	Lys	Ser	His	Lys	Thr 400
Arg	Asn	Gln	Asp	Glu 405	Gly	Ile	Leu	Pro	Ser 410	Gly	Arg	Arg	Gly	Thr 415	Ala
Arg	Gly	Pro	Ala	Arg 420											

<210> 45
<211> 23
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: Fwd Primer

<400> 45
tgccccaga gaaaccgtc aac 23

<210> 46
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Rev Primer

<400> 46
cgtgagtaca tcggagcggg cagag 25

<210> 47
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 47
tcaggcgcg cttgccaca cagctgtgat c 31

<210> 48
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 48
tcaggcgcg cttatctgg caggacctct 30

<210> 49
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 49
tcaggcgcg cgtgcccgcg gccgc 25

<210> 50
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 50
ataaggcgcg ccctggcagg acctctcg 28

<210> 51
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 51
tcaggcgcg cttgcccaca cagctgtgat c 31

<210> 52
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 52
tcagggcgcg ccttatctgg caggacctct 30

<210> 53
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 53

tcaggcgcg ctgcccgcg gcgc

25

<210> 54

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligonucleotide

<400> 54

ataaggcgcg ccctggcagg acctctcg

28